B. Load (handwritten)

RAW SEQUENCE LISTING   DATE: 04/11/2001
PATENT APPLICATION: US/09/635,521A   TIME: 09:10:09

Input Set : A:\seqlistcorr.txt
Output Set: N:\CRF3\04112001\I635521A.raw

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 3 <110> APPLICANT: Katherine Galvin and Laura A. Rudolph-Owen
 5 <120> TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR THE DIAGNOSIS
 6       AND TREATMENT OF CARDIOVASCULAR AND TUMORIGENIC
 7       DISEASE USING 4941
 9 <130> FILE REFERENCE: MNI-094
11 <140> CURRENT APPLICATION NUMBER: 09/635,521A
12 <141> CURRENT FILING DATE: 2000-08-09
14 <150> PRIOR APPLICATION NUMBER: 60/199,908
15 <151> PRIOR FILING DATE: 2000-04-26
17 <160> NUMBER OF SEQ ID NOS: 3
19 <170> SOFTWARE: PatentIn Ver. 2.0
21 <210> SEQ ID NO: 1
22 <211> LENGTH: 1362
23 <212> TYPE: DNA
24 <213> ORGANISM: Homo sapiens
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28 <222> LOCATION: (1)..(1359)
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33   1               5                  10                  15
35 cac agt cat gtc ccc gag ttt gag gtg gcc acc tgg atc aaa atc acc    96
36 His Ser His Val Pro Glu Phe Glu Val Ala Thr Trp Ile Lys Ile Thr
37              20                  25                  30
39 ctt att ctg gtg tac ctg atc atc ttc gtg atg ggc ctt ctg ggg aac   144
40 Leu Ile Leu Val Tyr Leu Ile Ile Phe Val Met Gly Leu Leu Gly Asn
41          35                  40                  45
43 agc gcc acc att cgg gtc acc cag gtg ctg cag aag aaa gga tac ttg   192
44 Ser Ala Thr Ile Arg Val Thr Gln Val Leu Gln Lys Lys Gly Tyr Leu
45      50                  55                  60
47 cag aag gag gtg aca gac cac atg gtg agt ttg gct tgc tcg gac atc   240
48 Gln Lys Glu Val Thr Asp His Met Val Ser Leu Ala Cys Ser Asp Ile
49   65                  70                  75                  80
51 ttg gtg ttc ctc atc ggc atg ccc atg gag ttc tac agc atc atc tgg   288
52 Leu Val Phe Leu Ile Gly Met Pro Met Glu Phe Tyr Ser Ile Ile Trp
53              85                  90                  95
55 aat ccc ctg acc acg tcc agc tac acc ctg tcc tgc aag ctg cac act   336
56 Asn Pro Leu Thr Thr Ser Ser Tyr Thr Leu Ser Cys Lys Leu His Thr
57             100                 105                 110
59 ttc ctc ttc gag gcc tgc agc tac gct acg ctg ctg cac gtg ctg aca   384
60 Phe Leu Phe Glu Ala Cys Ser Tyr Ala Thr Leu Leu His Val Leu Thr
61          115                 120                 125
63 ctc agc ttt gag cgc tac atc gcc atc tgt cac ccc ttc agg tac aag   432
64 Leu Ser Phe Glu Arg Tyr Ile Ala Ile Cys His Pro Phe Arg Tyr Lys
65      130                 135                 140
67 gct gtg tcg gga cct tgc cag gtg aag ctg ctg att ggc ttc gtc tgg   480
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 68 Ala Val Ser Gly Pro Cys Gln Val Lys Leu Leu Ile Gly Phe Val Trp
 69 145                 150             155             160
 71 gtc acc tcc gcc ctg gtg gca ctg ccc ttg ctg ttt gcc atg ggt act     528
 72 Val Thr Ser Ala Leu Val Ala Leu Pro Leu Leu Phe Ala Met Gly Thr
 73                 165             170             175
 75 gag tac ccc ctg gtg aac gtg ccc agc cac cgg ggt ctc act tgc aac     576
 76 Glu Tyr Pro Leu Val Asn Val Pro Ser His Arg Gly Leu Thr Cys Asn
 77                 180             185             190
 79 cgc tcc agc acc cgc cac cac gag cag ccc gag acc tcc aat atg tcc     624
 80 Arg Ser Ser Thr Arg His His Glu Gln Pro Glu Thr Ser Asn Met Ser
 81                 195             200             205
 83 atc tgt acc aac ctc tcc agc cgc tgg acc gtg ttc cag tcc agc atc     672
 84 Ile Cys Thr Asn Leu Ser Ser Arg Trp Thr Val Phe Gln Ser Ser Ile
 85     210             215             220
 87 ttc ggc gcc ttc gtg gtc tac ctc gtg gtc ctg ctc tcc gta gcc ttc     720
 88 Phe Gly Ala Phe Val Val Tyr Leu Val Val Leu Leu Ser Val Ala Phe
 89 225             230             235             240
 91 atg tgc tgg aac atg atg cag gtg ctc atg aaa agc cag aag ggc tcg     768
 92 Met Cys Trp Asn Met Met Gln Val Leu Met Lys Ser Gln Lys Gly Ser
 93                 245             250             255
 95 ctg gcc ggg ggc acg cgg cct ccg cag ctg agg aag tcc gag agc gaa     816
 96 Leu Ala Gly Gly Thr Arg Pro Pro Gln Leu Arg Lys Ser Glu Ser Glu
 97                 260             265             270
 99 gag agc agg acc gcc agg agg cag acc atc atc ttc ctg agg ctg att     864
100 Glu Ser Arg Thr Ala Arg Arg Gln Thr Ile Ile Phe Leu Arg Leu Ile
101             275             280             285
103 gtt gtg aca ttg gcc gta tgc tgg atg ccc aac cag att cgg agg atc     912
104 Val Val Thr Leu Ala Val Cys Trp Met Pro Asn Gln Ile Arg Arg Ile
105     290             295             300
107 atg gct gcg gcc aaa ccc aag cac gac tgg acg agg tcc tac ttc cgg     960
108 Met Ala Ala Ala Lys Pro Lys His Asp Trp Thr Arg Ser Tyr Phe Arg
109 305             310             315             320
111 gcg tac atg atc ctc ctc ccc ttc tcg gag acg ttt ttc tac ctc agc    1008
112 Ala Tyr Met Ile Leu Leu Pro Phe Ser Glu Thr Phe Phe Tyr Leu Ser
113                 325             330             335
115 tcg gtc atc aac ccg ctc ctg tac acg gtg tcc tcg cag cag ttt cgg    1056
116 Ser Val Ile Asn Pro Leu Leu Tyr Thr Val Ser Ser Gln Gln Phe Arg
117                 340             345             350
119 cgg gtg ttc gtg cag gtg ctg tgc tgc cgc ctg tcg ctg cag cac gcc    1104
120 Arg Val Phe Val Gln Val Leu Cys Cys Arg Leu Ser Leu Gln His Ala
121             355             360             365
123 aac cac gag aag cgc ctg cgc gta cat gcg cac tcc acc acc gac agc    1152
124 Asn His Glu Lys Arg Leu Arg Val His Ala His Ser Thr Thr Asp Ser
125     370             375             380
127 gcc cgc ttt gtg cag cgc ccg ttg ctc ttc gcg tcc cgg cgc cag tcc    1200
128 Ala Arg Phe Val Gln Arg Pro Leu Leu Phe Ala Ser Arg Arg Gln Ser
129 385             390             395             400
131 tct gca agg aga act gag aag att ttc tta agc act ttt cag agc gag    1248
132 Ser Ala Arg Arg Thr Glu Lys Ile Phe Leu Ser Thr Phe Gln Ser Glu
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133                    405            410            415
135 gcc gag ccc cag tct aag tcc cag tca ttg agt ctc gag tca cta gag   1296
136 Ala Glu Pro Gln Ser Lys Ser Gln Ser Leu Ser Leu Glu Ser Leu Glu
137                    420            425            430
139 ccc aac tca ggc gcg aaa cca gcc aat tct gct gca gag aat ggt ttt   1344
140 Pro Asn Ser Gly Ala Lys Pro Ala Asn Ser Ala Ala Glu Asn Gly Phe
141          435            440            445
143 cag gag cat gaa gtt tga                                            1362
144 Gln Glu His Glu Val
145      450
148 <210> SEQ ID NO: 2
149 <211> LENGTH: 453
150 <212> TYPE: PRT
151 <213> ORGANISM: Homo sapiens
153 <400> SEQUENCE: 2
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157 His Ser His Val Pro Glu Phe Glu Val Ala Thr Trp Ile Lys Ile Thr
158              20             25             30
160 Leu Ile Leu Val Tyr Leu Ile Ile Phe Val Met Gly Leu Leu Gly Asn
161          35             40             45
163 Ser Ala Thr Ile Arg Val Thr Gln Val Leu Gln Lys Lys Gly Tyr Leu
164      50             55             60
166 Gln Lys Glu Val Thr Asp His Met Val Ser Leu Ala Cys Ser Asp Ile
167  65             70             75             80
169 Leu Val Phe Leu Ile Gly Met Pro Met Glu Phe Tyr Ser Ile Ile Trp
170              '85             90             95
172 Asn Pro Leu Thr Thr Ser Ser Tyr Thr Leu Ser Cys Lys Leu His Thr
173          100            105            110
175 Phe Leu Phe Glu Ala Cys Ser Tyr Ala Thr Leu Leu His Val Leu Thr
176          115            120            125
178 Leu Ser Phe Glu Arg Tyr Ile Ala Ile Cys His Pro Phe Arg Tyr Lys
179      130            135            140
181 Ala Val Ser Gly Pro Cys Gln Val Lys Leu Leu Ile Gly Phe Val Trp
182 145            150            155            160
184 Val Thr Ser Ala Leu Val Ala Leu Pro Leu Leu Phe Ala Met Gly Thr
185              165            170            175
187 Glu Tyr Pro Leu Val Asn Val Pro Ser His Arg Gly Leu Thr Cys Asn
188          180            185            190
190 Arg Ser Ser Thr Arg His His Glu Gln Pro Glu Thr Ser Asn Met Ser
191          195            200            205
193 Ile Cys Thr Asn Leu Ser Ser Arg Trp Thr Val Phe Gln Ser Ser Ile
194      210            215            220
196 Phe Gly Ala Phe Val Val Tyr Leu Val Val Leu Leu Ser Val Ala Phe
197 225            230            235            240
199 Met Cys Trp Asn Met Met Gln Val Leu Met Lys Ser Gln Lys Gly Ser
200              245            250            255
202 Leu Ala Gly Gly Thr Arg Pro Pro Gln Leu Arg Lys Ser Glu Ser Glu
203          260            265            270
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205 Glu Ser Arg Thr Ala Arg Arg Gln Thr Ile Ile Phe Leu Arg Leu Ile
206         275             280             285
208 Val Val Thr Leu Ala Val Cys Trp Met Pro Asn Gln Ile Arg Arg Ile
209     290             295             300
211 Met Ala Ala Ala Lys Pro Lys His Asp Trp Thr Arg Ser Tyr Phe Arg
212 305             310             315             320
214 Ala Tyr Met Ile Leu Leu Pro Phe Ser Glu Thr Phe Phe Tyr Leu Ser
215             325             330             335
217 Ser Val Ile Asn Pro Leu Leu Tyr Thr Val Ser Ser Gln Gln Phe Arg
218             340             345             350
220 Arg Val Phe Val Gln Val Leu Cys Cys Arg Leu Ser Leu Gln His Ala
221         355             360             365
223 Asn His Glu Lys Arg Leu Arg Val His Ala His Ser Thr Thr Asp Ser
224     370             375             380
226 Ala Arg Phe Val Gln Arg Pro Leu Leu Phe Ala Ser Arg Arg Gln Ser
227 385             390             395             400
229 Ser Ala Arg Arg Thr Glu Lys Ile Phe Leu Ser Thr Phe Gln Ser Glu
230             405             410             415
232 Ala Glu Pro Gln Ser Lys Ser Gln Ser Leu Ser Leu Glu Ser Leu Glu
233             420             425             430
235 Pro Asn Ser Gly Ala Lys Pro Ala Asn Ser Ala Ala Glu Asn Gly Phe
236             435             440             445
238 Gln Glu His Glu Val
239         450
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243 <211> LENGTH: 2528
244 <212> TYPE: DNA
245 <213> ORGANISM: Homo sapiens
247 <220> FEATURE:
248 <221> NAME/KEY: CDS
249 <222> LOCATION: (42)..(1400)
251 <220> FEATURE:
252 <223> OTHER INFORMATION: N at positions 2490 and 2493 may be Adenine,
253         Guanine, Cytosine or Thymine
255 <400> SEQUENCE: 3
256 gggagtcgac ccacgcgtcc ggtagcctgg tgctctttct c atg gct tca ccc agc 56
257                                             Met Ala Ser Pro Ser
258                                             1               5
260 ctc ccg ggc agt gac tgc tcc caa atc att gat cac agt cat gtc ccc   104
261 Leu Pro Gly Ser Asp Cys Ser Gln Ile Ile Asp His Ser His Val Pro
262                 10              15              20
264 gag ttt gag gtg gcc acc tgg atc aaa atc acc ctt att ctg gtg tac   152
265 Glu Phe Glu Val Ala Thr Trp Ile Lys Ile Thr Leu Ile Leu Val Tyr
266             25              30              35
268 ctg atc atc ttc gtg atg ggc ctt ctg ggg aac agc gcc acc att cgg   200
269 Leu Ile Ile Phe Val Met Gly Leu Leu Gly Asn Ser Ala Thr Ile Arg
270             40              45              50
272 gtc acc cag gtg ctg cag aag aaa gga tac ttg cag aag gag gtg aca   248
273 Val Thr Gln Val Leu Gln Lys Lys Gly Tyr Leu Gln Lys Glu Val Thr
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RAW SEQUENCE LISTING   DATE: 04/11/2001
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Input Set : A:\seqlistcorr.txt
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274       55                    60                    65
276 gac cac atg gtg agt ttg gct tgc tcg gac atc ttg gtg ttc ctc atc    296
277 Asp His Met Val Ser Leu Ala Cys Ser Asp Ile Leu Val Phe Leu Ile
278  70                    75                    80                    85
280 ggc atg ccc atg gag ttc tac agc atc atc tgg aat ccc ctg acc acg    344
281 Gly Met Pro Met Glu Phe Tyr Ser Ile Ile Trp Asn Pro Leu Thr Thr
282                    90                    95                   100
284 tcc agc tac acc ctg tcc tgc aag ctg cac act ttc ctc ttc gag gcc    392
285 Ser Ser Tyr Thr Leu Ser Cys Lys Leu His Thr Phe Leu Phe Glu Ala
286                   105                   110                   115
288 tgc agc tac gct acg ctg ctg cac gtg ctg aca ctc agc ttt gag cgc    440
289 Cys Ser Tyr Ala Thr Leu Leu His Val Leu Thr Leu Ser Phe Glu Arg
290                   120                   125                   130
292 tac atc gcc atc tgt cac ccc ttc agg tac aag gct gtg tcg gga cct    488
293 Tyr Ile Ala Ile Cys His Pro Phe Arg Tyr Lys Ala Val Ser Gly Pro
294        135                   140                   145
296 tgc cag gtg aag ctg ctg att ggc ttc gtc tgg gtc acc tcc gcc ctg    536
297 Cys Gln Val Lys Leu Leu Ile Gly Phe Val Trp Val Thr Ser Ala Leu
298 150                   155                   160                   165
300 gtg gca ctg ccc ttg ctg ttt gcc atg ggt act gag tac ccc ctg gtg    584
301 Val Ala Leu Pro Leu Leu Phe Ala Met Gly Thr Glu Tyr Pro Leu Val
302                   170                   175                   180
304 aac gtg ccc agc cac cgg ggt ctc act tgc aac cgc tcc agc acc cgc    632
305 Asn Val Pro Ser His Arg Gly Leu Thr Cys Asn Arg Ser Ser Thr Arg
306                   185                   190                   195
308 cac cac gag cag ccc gag acc tcc aat atg tcc atc tgt acc aac ctc    680
309 His His Glu Gln Pro Glu Thr Ser Asn Met Ser Ile Cys Thr Asn Leu
310                   200                   205                   210
312 tcc agc cgc tgg acc gtg ttc cag tcc agc atc ttc ggc gcc ttc gtg    728
313 Ser Ser Arg Trp Thr Val Phe Gln Ser Ser Ile Phe Gly Ala Phe Val
314        215                   220                   225
316 gtc tac ctc gtg gtc ctg ctc tcc gta gcc ttc atg tgc tgg aac atg    776
317 Val Tyr Leu Val Val Leu Leu Ser Val Ala Phe Met Cys Trp Asn Met
318 230                   235                   240                   245
320 atg cag gtg ctc atg aaa agc cag aag ggc tcg ctg gcc ggg ggc acg    824
321 Met Gln Val Leu Met Lys Ser Gln Lys Gly Ser Leu Ala Gly Gly Thr
322                   250                   255                   260
324 cgg cct ccg cag ctg agg aag tcc gag agc gaa gag agc agg acc gcc    872
325 Arg Pro Pro Gln Leu Arg Lys Ser Glu Ser Glu Glu Ser Arg Thr Ala
326                   265                   270                   275
328 agg agg cag acc atc atc ttc ctg agg ctg att gtt gtg aca ttg gcc    920
329 Arg Arg Gln Thr Ile Ile Phe Leu Arg Leu Ile Val Val Thr Leu Ala
330                   280                   285                   290
332 gta tgc tgg atg ccc aac cag att cgg agg atc atg gct gcg gcc aaa    968
333 Val Cys Trp Met Pro Asn Gln Ile Arg Arg Ile Met Ala Ala Ala Lys
334        295                   300                   305
336 ccc aag cac gac tgg acg agg tcc tac ttc cgg gcg tac atg atc ctc   1016
337 Pro Lys His Asp Trp Thr Arg Ser Tyr Phe Arg Ala Tyr Met Ile Leu
338 310                   315                   320                   325
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Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the
Sequence Listing to ensure that a corresponding explanation is presented in the <220> to
<223> fields of each sequence which presents at least one n or Xaa.

VERIFICATION SUMMARY   DATE: 04/11/2001
PATENT APPLICATION: US/09/635,521A   TIME: 09:10:11

Input Set : A:\seqlistcorr.txt
Output Set: N:\CRF3\04112001\I635521A.raw

L:408 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3